



8/13

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 1098,600A
Source: OPE
Date Processed by STIC: 8/13/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Revised 01/29/2002



OIPE

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 08/13/2002

PATENT APPLICATION: US/10/098,600A

TIME: 13:56:23

Input Set : A:\Corrected Seq Listing.txt

Output Set: N:\CRF3\08132002\J098600A.raw

5 <110> APPLICANT: Messier, Walter
 7 Sikela, James M
 11 <120> TITLE OF INVENTION: Methods to Identify Polynucleotide and Polypeptide
 13 Sequences Which May Be Associated with Physiological
 15 and Medical Conditions
 19 <130> FILE REFERENCE: GENO2002CIP2
 C--> 23 <140> CURRENT APPLICATION NUMBER: US/10/098,600A
 C--> 25 <141> CURRENT FILING DATE: 2002-03-14
 29 <150> PRIOR APPLICATION NUMBER: 09/591,435
 31 <151> PRIOR FILING DATE: 2000-06-09
 35 <150> PRIOR APPLICATION NUMBER: 09/240,915
 37 <151> PRIOR FILING DATE: 1999-01-29
 41 <150> PRIOR APPLICATION NUMBER: 60/073,263
 43 <151> PRIOR FILING DATE: 1998-01-30
 47 <150> PRIOR APPLICATION NUMBER: 60/098,987
 49 <151> PRIOR FILING DATE: 1998-09-02
 53 <150> PRIOR APPLICATION NUMBER: 09/942,252
 55 <151> PRIOR FILING DATE: 2001-08-28
 E--> 59 <160> NUMBER OF SEQ ID NOS: (33) — counted 36
 63 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

See p. 2 for other errors

VARIABLE LOCATION SUMMARY

DATE: 08/13/2002

PATENT APPLICATION: US/10/098,600A

TIME: 13:56:24

Input Set : A:\Corrected Seq Listing.txt

Output Set: N:\CRF3\08132002\J098600A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:32; Xaa Pos. 71

Seq#:33; Xaa Pos. 71

VERIFICATION SUMMARY

DATE: 08/13/2002

PATENT APPLICATION: US/10/098,600A

TIME: 13:56:24

Input Set : A:\Corrected Seq Listing.txt

Output Set: N:\CRF3\08132002\J098600A.raw

L:23 M:270 C: Current Application Number differs, Replaced Application Number
L:25 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:4061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:240
L:4293 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:4293 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:4293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:64
L:4785 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:35
L:59 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (33) Counted (36)